Distribution of C3 Phenotypes in North India: A Pilot Study

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Summary. The commonly occurring phenotypes and some rare variants of C3 were studied in a North Indian population. Based on known gene frequencies, the Indian population seemed more akin to Mongol, African, and Afghan populations than to Caucasians.

Introduction

Since the genetically determined polymorphism of the complement protein C3 (β C globulin) has been established (Alper and Propp, 1968; Azen and Smithies, 1968), gene frequencies of the alleles governing the third component of complement have been studied in a number of populations. Most of these investigations have been of Caucasians and Africans. Only one report is available on C3 polymorphism in Japan (Harada et al., 1975) and another on four different populations in Afghanistan (Agarwal et al., 1976). To the best of our knowledge, this investigation is the first of its kind on an Indian population. Our reasons for making this investigation were twofold: firstly, to determine a marker for population studies in Asiatic populations and compare this with other populations; and second, to use this marker as a point of comparison between healthy and diseased populations in future studies.

Materials and Methods

Serum samples were obtained from a random population in and around Delhi, and either used immediately or stored at -20°C. Sera of 290 unrelated adults were investigated for this study.

Agarose Gel Electrophoresis. 30 ml of 1% agarose layered on glass plates (21 x 11 cm) were subjected to high-voltage electrophoresis in order to phenotype C3 following the method of Teisberg (1970). Gels were stained in 2% amido black in a methanol, water, and acetic acid mixture (2:2:1).

Variants of C3^F and C3^S were computed according to Rittner and Rittner (1974).

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Results and Discussion

C3 Phenotypes and the distribution of gene frequencies in the sample under study are shown in Table 1. It is seen that observed and expected values for the distribution of various phenotypes were in good agreement ($\chi^2 = 0.06296$). Besides the common phenotypes SS, FS, and FF, fourteen rare variants were identified, mostly the phenotype SS0.4. An interesting case was that of a phenotype with one possible silent gene, S, which was seen in repeated runs. Unfortunately, the parents could not be tested and therefore the origin of the missing allele could not be traced. Moreover, activity determinations could not be performed.

Our results show a high incidence of C3S in the Indian population. This has special significance in view of the fact that all Oriental populations studied have shown a much higher frequency for C3S than American and European populations (Alper and Propp, 1968; Farhud and Walter, 1973; Harada et al., 1975; Agarwal et al., 1976).

In Table 2 we have compiled some gene frequencies for Caucasian, African, and Oriental populations reported by various authors. The distinct differences in allele frequency among the major races suggest that the C3F gene is most common in Caucasians and least so in Orientals, while the S gene occurs in all three major races of mankind, i.e., the Caucasian, Oriental, and Negroid races (Seth and Seth, 1976). Most Caucasian populations have a strikingly similar gene frequency for the C3S gene (usually between 17—21%) with the exception of the Lapps (Teisberg, 1971), where the gene frequency is between 3—7%, as in other non-Caucasians (Bronnestam, 1973).

The C3S allele is less common in European populations than in African (Kuhnl and Spielman, 1972; Farhud and Walter, 1973b), Afghan (Agarwal et al., 1976), Mongoloid (Alper and Propp, 1968; Harada et al., 1975), and Indian populations (present study). Based on known gene frequencies in African, Mongol, and Afghan populations, the Indian population seems closer to them than to the Caucasian stock. Such a conclusion can at best serve as an indication, as the number of studies on a population is sometimes limited to only one. To make a meaningful analysis, several populations in various regions of Asia must be studied. The Indian population needs to be studied on the basis of caste, because this factor strongly governs the confines of marriage, and intercaste marriages are uncommon.

It will be interesting, for instance, to compare relative gene frequencies in certain north Indian populations, such as that of Punjab (which is thought to be 'Aryan' and therefore of Caucasian stock) and some south Indian populations like the Brahmins of Tamil Nadu, who are a closely inbreeding people of Dravidian stock. In this context, our investigation serves as a pilot study on an Indian population and we propose to make detailed investigations on sub-populations based on caste.

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